



SEQUENCE LISTING

<110> Wands, Jack R.

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<120> DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

<130> 21486-032 CIP

<140> USSN 09/859,604

<141> 2001-05-17

<150> 09/436,184

<151> 1999-11-08

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
EGF-like domain

<220>

<221> VARIANT

<222> (2)..(8)

<223> Wherein any Xaa may be any amino acid

<220>

<221> VARIANT

<222> (10)..(13)

<223> Wherein Xaa is any amino acid.

<220>

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<222> (15)..(24)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (26)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (28)..(35)

<223> Wherein Xaa is any amino acid.

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Cys
35

<210> 2

<211> 758

<212> PRT

<213> Homo sapiens

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Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
20 25 30

Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
35 40 45

Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
50 55 60

Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
65 70 75 80

Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
85 90 95

Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
100 105 110

Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
115 120 125

Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
 130 135 140

Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
 145 150 155 160

Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr
 165 170 175

Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
 180 185 190

Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
 195 200 205

Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
 210 215 220

Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
 225 230 235 240

Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
 245 250 255

Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
 260 265 270

Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
 275 280 285

Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
 290 295 300

Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
 305 310 315 320

Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys
 325 330 335

Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
 340 345 350

Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val
 355 360 365

Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys
 370 375 380

Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly
 385 390 395 400
 Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala
 405 410 415
 Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe
 420 425 430
 Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln
 435 440 445
 Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr
 450 455 460
 Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Glu Val
 465 470 475 480
 Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe
 485 490 495
 Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys
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 Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr
 515 520 525
 Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr
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 Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp
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 Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp
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 Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg
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 Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp
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Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu
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Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro
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Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg
675 680 685

Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys
690 695 700

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Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu
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Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg
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Arg Ser Leu Pro Ala Ile
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<211> 2324

<212> DNA

<213> Homo sapiens

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<211> 31

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: EGF-like
cysteine-rich repeat

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<221> VARIANT

<222> (2)..(5)

<223> Wherein any Xaa may be any amino acid

<220>

<221> VARIANT

<222> (7)..(8)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (10)

<223> Wherein Xaa is any amino acid.

<220>
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<220>
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<220>
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<220>
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 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys
 20 25 30

<210> 5
 <211> 1242
 <212> PRT
 <213> Homo sapiens

<400> 5
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 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
 20 25 30
 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
 35 40 45
 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
 50 55 60
 Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn
 65 70 75 80

Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala
 85 90 95

Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln
 100 105 110

Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly
 115 120 125

Ala Gly Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu
 130 135 140

Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe
 145 150 155 160

Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr
 165 170 175

Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile
 180 185 190

Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu
 195 200 205

Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu
 210 215 220

Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val
 225 230 235 240

Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala
 245 250 255

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser
 260 265 270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His
 275 280 285

Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg
 290 295 300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys
 305 310 315 320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met
 325 330 335

Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn
 340 345 350

Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro
 355 360 365

Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro
 370 375 380

Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Ser Thr Ser Gly His
 385 390 395 400

Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val
 405 410 415

Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly
 420 425 430

Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp
 435 440 445

Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Glu Leu Ser Asn
 450 455 460

Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn
 465 470 475 480

Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro
 485 490 495

Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala
 500 505 510

Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala
 515 520 525

Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser
 530 535 540

Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro
 545 550 555 560

Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe
 565 570 575

Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu
 580 585 590

Glu	Arg	Arg	Gly	Gly	His	His	Arg	Pro	Asp	Ser	Ser	Thr	Leu	His	Thr	595	600	605	
Asp	Asp	Gly	Tyr	Met	Pro	Met	Ser	Pro	Gly	Val	Ala	Pro	Val	Pro	Ser	610	615	620	
Gly	Arg	Lys	Gly	Ser	Gly	Asp	Tyr	Met	Pro	Met	Ser	Pro	Lys	Ser	Val	625	630	635	640
Ser	Ala	Pro	Gln	Gln	Ile	Ile	Asn	Pro	Ile	Arg	Arg	His	Pro	Gln	Arg	645	650	655	
Val	Asp	Pro	Asn	Gly	Tyr	Met	Met	Met	Ser	Pro	Ser	Gly	Gly	Cys	Ser	660	665	670	
Pro	Asp	Ile	Gly	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asn	Ala	675	680	685	
Val	Pro	Ser	Gly	Thr	Ser	Tyr	Gly	Lys	Leu	Trp	Thr	Asn	Gly	Val	Gly	690	695	700	
Gly	His	His	Ser	His	Val	Leu	Pro	His	Pro	Lys	Pro	Pro	Val	Glu	Ser	705	710	715	720
Ser	Gly	Gly	Lys	Leu	Leu	Pro	Cys	Thr	Gly	Asp	Tyr	Met	Asn	Met	Ser	725	730	735	
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Pro	Glu	Asp	Pro	Gln	His	Lys	Pro	Val	Leu	Ser	Tyr	Tyr	Ser	Leu	Pro	755	760	765	
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Gly	Gly	Gly	Tyr	Cys	Gly	Ala	Arg	Leu	Glu	Pro	Ser	Leu	Pro	His	Pro	820	825	830	
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Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly
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Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln Gln
 865 870 875 880

Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr
 885 890 895

Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro
 900 905 910

Val Ala Phe His Ser Ser Pro Ser Val Arg Cys Pro Ser Gln Leu Gln
 915 920 925

Pro Ala Pro Arg Glu Glu Glu Thr Gly Thr Glu Glu Tyr Met Lys Met
 930 935 940

Asp Leu Gly Pro Gly Arg Arg Ala Ala Trp Gln Glu Ser Thr Gly Val
 945 950 955 960

Glu Met Gly Arg Leu Gly Pro Ala Pro Pro Gly Ala Ala Ser Ile Cys
 965 970 975

Arg Pro Thr Arg Ala Val Pro Ser Ser Arg Gly Asp Tyr Met Thr Met
 980 985 990

Gln Met Ser Cys Pro Arg Gln Ser Tyr Val Asp Thr Ser Pro Ala Ala
 995 1000 1005

Pro Val Ser Tyr Ala Asp Met Arg Thr Gly Ile Ala Ala Glu Glu Val
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Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg His Ser Ser Glu Thr Phe
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Ala Gly Ala Ala Val Gly Gly Gly Gly Gly Ser Ser Ser Ser Ser Glu
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Asp Val Lys Arg His Ser Ser Ala Ser Phe Glu Asn Val Trp Leu Arg
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Pro Pro Pro Pro Pro Pro Pro His Gln Pro Leu Gly Ser Gly Glu Ser
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 <212> DNA
 <213> Homo sapiens

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